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Title:
Perfect score:
Sequence:
                                                        Scoring table:
                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
      Searched:
                                                                                                                                                                                                                       Run on:
                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                 US-09-831-805A-6
1635
1 MALRRPPRLRLCARLPDFFL......VNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                            December 15, 2003, 14:50:12 ; Search time 21 Seconds (without alignments)
1419.633 Million cell updates/sec
283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

N.	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	vo	80	7	6	u	4	w	N		Result No.
	155.		155.								159.5	161	161.5	162.5	163	164		169	170.5	171.5	171.5	177	177	180	180.5	186	187	419	Score
9.	9.5	9.5			9.5		9.6	9.7	9.7	9.7	٠	9.8	9.9	9.9	10.0	10.1	10.1	10.4	10.4	0	10.5	0	0		11.0	11.4	11.4	25.6	Query Match
495	1268	1259	761	1863	1501	1091	1907	4162	1323	538	1033	7962	1612	6642	853	3707	1051	1912	858	1115	725	1092	725	333	1894	1088	725	299	Length
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T25750	A39640	A43425	IJHUNG	S46217	I58148	IJCHNL	850893	T42633	B950Nd	JC2457	S19247	I38346	T30805	T29757	IJBONC	S18252	A39712	A56178	IJRTNC	IJMSNL	IJMSNG	JN0635	JE0100	A31923	C54689	IJXLNL	JE0099	S56749	Ħ
nypothetical prote	O)	Bravo/Nr-CAM cell	neural cell adhesi	protein-tyrosine-p	protein-tyrosine-p	neural cell adhesi	protein-tyrosine-p	connectin/titin -	connectin 3B - chi	vascular cell adhe	-	Ε.	н	protein UNC-89 - C	cell adhe	heparan sulfate pr	kinase-like protei	protein-tyrosine-p	neural cell adhesi	-	_	cell	cell adhe	am protein p	ä	cell	neural cell adhesi	al adhes	Description

45	4 4	4	42	41	40	39	8	37	36	ω G	34	33	32	31	30
147	147	147.5	147.5	148.5	149	149	149.5	150	150	150.5	151	152	153	153	153.5
9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.2	9.2	9.2	9.2	9.3	9.4	9.4	9.4
344	338	881	871	646	1898	521	1897	1496	1262	702	1651	483	875	352	365
N	N	_	μ	N	N	N	ب	_	μ	N	N	N	N	N	N
156551	JC5519	I48697	I48696	I38049	S46216	S34338	TDHULK	A48758	B48758	A36319	T14160	T17346	T33434	T33433	JC7780
neurotrimin - rat	50K glycoprotein p	protein-tyrogine k	protein-tyrosine k	cell surface glyco	leukocyte antigen-	biliary glycoprote	leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	carcinoembryonic a	transmembrane rece	hypothetical prote	hypothetical prote	hypothetical prote	coxsackie- and ade

ALIGNMENTS

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8	g &	P 68	B 6	B 8	Query Match Best Local : Matches 10:	A;Note: the C;Genetics: A;Gene: JAM C;Keywords: F;1-25/Doma: F;26-299/Pro	A;Title: A;Refere A;Access A;Molecu A;Residu	A;Status: I A;Molecule A;Residues A;Cross-rei R;Naik, U.I Biochem. J	RESULT 1 \$56749 junction N,Altern C;Specie C;Access R;Ozaki, J. Immun A;Title: A;Refers A;Access
	188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246 	128 EIVIELTVQVKPVTBVCRVPKAVPVGKMATLHCQESEGHPRDHYSWYRNDVPLPTDSRAN 187 	68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127 	8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67	Query Match 25.6%; Score 419; DB 2; Length 299; Best Local Similarity 32.8%; Pred. No. 3e-27; Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;	A;Note: the order of the peptides other than the amino terminus was not determined C;Genetics: C;Genetics: A;Gene: JAM C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrar F;1-25/Domain: signal sequence #status predicted <sig> F;1-299/Product: junctional adhesion molecule #status predicted <mat></mat></sig>	A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a A;Reference number: S56749; MUID:95374438; PMID:7646439 A;Reference number: S56749 A;Rolecule type: protein A;Residues: 28-49, X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X'	ry 52A> CB:AAD42050; NID:g5326797; PIDN:AAD42050.1 Ch, Y.H.; Kornecki, E. 5-162, 1995	RESULT 1 S56749 S156749 Synctional adhesion molecule precursor - human junctional adhesion molecule precursor - human junctional adhesion molecule precursor - human like procursor - human supplemental platelet antigen; platelet adhesion molecule procure platelet F11 C; Species: Homo sapiens (man) C; Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C; Accession: A59406; S56749 C; Accession: A59406; Noriuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K J. Immunol. 163, 553-557, 1999 J. Immunol. 163, 553-557, 1999 A; Fitle: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution; Reference number: A59406; MUID:99323940; PMID:10395639 A; Recession: A59406

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A;Gene: NCAM
C;Superfamily
C;Keywords: a
F;1-19/Domain
                                                                                                                                                                                                                                      R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-1033.
A;Title: Primary structure and developmental expression
A;Reference number: S09600; MUID:90098871; PMID:2481269
                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain C;Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incural cell adhesion molecule 1 - African N,Alternate names: N-CAM 1 C;Species: Xenopus laevis (African clawed C;Date: 19-May-1998 #sequence_revision 29-C;Accession: JE0099 R;Kudo, M.; Takayama, E.; Tadakuma, T.; Sh Biochem. Biophys. Res. Commun. 245, 127-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A; Title: Molecular cloning of ssd-form neural cell adhesion
A; Reference number: JE0099; MUID:98204770; PMID:9535795
                                                                                                                                                                                                                                                                                                                                                                                                                   neural cell adhesion molecule long domain
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A;Experimental source: heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JE0099
Superfamily: neural cell adhesion molecule; Keywords: alternative splicing; brain; cell; 1-19/Domain: signal sequence #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                     Accession: S09600
                                                                                                                                                                                                                                                                                                                                    Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512-589/Domain: fibronectin type III repeat homology <3FR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DV-----RFVVLANNYLQİRGIKKTDEGTYRCEGRILARGEINYKDIQVİVNVPPTIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAVNIK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDOSEMTIHHVEKDDEAEYSCIANNOAGEA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQTSSFLV 299
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      predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187; DB 2;
No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                 form precursor -
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                    adhesion;
                                          fibronectin
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                    in type III repeat homology; is
duplication; heparin binding;
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F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TNM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;724-1088/Domain: intracellular #status predicted obods: #status predicted
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
261
                                                        198
                                                                                                                                                                                                                                   160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              63;
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                                                                                                                                                                                                                                                                                                                                                                                                        GAVNLK----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN
                                               NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
                                                                                                                                                                    KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHL 197
                                                                                                                                                                                                                             DV-----RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA
                                                                                                                                                                                                                                                                                KIQGDLAGRABILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDBIV-IBLTVQV 137
                                                                                                                                                                                                                                                                                                                                               GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159
NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                              -RVNATANMAESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 186; DB 1;
Pred. No. 3.1e-07;
0; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1088,
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                                                                                                                 260
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                                                                                                                                                                                                                                213
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RESULT 4 C54689

A;Note: C;Superf C;Species: Mis musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_chan;
C;Accession: C54689; B54689
R,Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikav Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, A;Reference number: A54689; MUID:93360986; PMID:8355897
A;Accession: C54689 A;Experimental source: brain; splice form B A;Note: sequence inconsistent with nucleotide A;Note: sequence extracted from NCBI backbone B:Arcasion. Bearing A;Experimental source: brain; splice form C
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, A; Molecule type: mRNA A; Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2> A;Status: preliminary A; Accession: B54689 A; Molecule type: mRNA A; Residues: 1-1894 < MIZ> protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form N;Alternate names: MPTP delta type B/C N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C N;Contains: $\frac{1}{2}$ A;Status: preliminary Superfamily: leukocyte antigen-related protein; translation (NCBIN:137486, fibronectin #text_change Ichikawa, NCBIP: 136530) NCBIP: 137487) type BT expressed in 12-Feb-1999 T.; Yakura, III repeat homology; W Ξ ф precursor ize

C; Keywords: allerne.

C; Keywords: allerne.

F; 45-107/Domain: immunoglobulin homology <IMM2>
F; 245-299/Domain: immunoglobulin homology <IMM2>
F; 217-399/Domain: fibronectin type III repeat homology <FN3A>
F; 317-399/Domain: fibronectin type III repeat homology <FN3A>
F; 1278-1894/Domain: leukocyte common antigen cytosolic domain homology <L
F; 1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F: 1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F: 1636/Active site: Cys (phosphocysteine intermediate) #status predicted

phosphoric

monoester

hyc

V

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neural cell adhesion molecule 2 - African clawed frog
N;Alternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
                                                    RESULT
JE0100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amalgam protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-333 <SEE>
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                                                                                                                                                         GOYYCIASNDAGSA 228
                                                                                                                                                                                            SAELEC-SVOGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEEDF
                                                                                                                                                                                                                            MATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDS 214
                                                                                                                                                                                                                                                                                             LGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECVÁTNSÁGT 216
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                                                                                                                          GDYYCNATNKLGHA
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                                                                                                                                                                                                                                                                                                                                                                                                    39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180; DB 2;
Pred. No. 2.3e-07;
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F;129-188/Domain: immunoglobulin homology < IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;317-381/Domain: immunoglobulin homology < IMM3>
F;413-475/Domain: immunoglobulin homology < IMM4>
F;512-89/Domain: fibronectin type III repeat homology <FN3A>
F;512-89/Domain: fibronectin type III repeat homology <FN3B>
F;716-733/Domain: transmembrane #status predicted < IMM>
F;724-1092/Domain: intracellular #status predicted < IMT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
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C;Accession: JE0100
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion
A;Reference number: JE0099; MUID:98204770; PMID:9535795
                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunof;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc F;1-19/Domain: signal sequence #status predicted csis; F;20-1092/Product: neural cell adhesion molecule 2 #status predicted cNCA> F;20-705/Domain: extracellular #status predicted cEXT> F;34-95/Domain: immunoglobulin homology <IMM1>
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F;512-589/Domain: fibronectin type III repeat homology <3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: NCAM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1092 <TON>
A; Cross-references: GB:M76710; NID:g214611;
C; Comment: NCAM mediates cell-cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 127, 243-247, 1993
A;Title: Two neural-cell adhesion molecule(NCAM)-encoding
A;Reference number: JN0635; MUID:93273239; PMID:7684721
A;Accession: JN0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: JN0635
R; Tonissen, K.F.; Krieg, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neural cell adhesion molecule 2 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
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A; Residues: 1-725 < KUD>
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,310,341,417,443,472/Binding site: carbohydrate (Asn)
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Pred. No. 1.1e-06;
8; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAA49910.1; PID:g214612 via homophilic binding with
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10.8%;

Score 177;

DB 1;

Length 1092;

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A; Molecule type: protein A; Residues; 20-36 < ROU's C; Comment: NCAM mediates c C; Comment: Several forms C; Genetics:
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A; Introns: 701/1
C; Superfamily: neux
C; Keywords: alterna
F; 1-19/Domain: sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunologica
A;Reference number: A44290; MUID:861
A;Accession: A44290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; F R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C. EMBO J., 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00382
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-193 #sequence revisio
C;Accession: A29673; S00382; A44290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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A; Residues: 642-656, 'D', 658-725
A; Cross-references: EMBL: X07195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, EMBO J. 6, 907-914, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neural cell adhesion molecule 1 precursor,
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                                                                                                      152-156/Region: heparin binding #status predicted
161-165/Region: heparin binding #status predicted
1228-290/Domain: immunoglobulin homology <IMM3
1263-272/Region: NCAM binding #status predicted
1263-272/Region: NCAM binding #status predicted
1263-388/Domain: immunoglobulin homology <IMM4
1264-1262/Domain: immunoglobulin homology <IMM5
1265-586/Domain: fibronectin type III repeat homology <FN3A
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
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1265-685/Domain: fibronectin type III repeat homology <FN3B
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1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
1265-685/Domain: fibronectin type III repeat homology <FN3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immn; Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane; 1-19/Domain: signal sequence #status predicted <SIG>; 34-98/Domain: immunoglobulin homology <IMNI; 194-98/Domain: immunoglobulin <IMNI; 194-98/Domain: immunoglobulin <IMNI; 194-98/Domain: immunoglobulin <IMNI; 194-98/Domain: immunoglobulin <IMNI; 194-98/Domain: immunoglobulin <IMNI; 194-98/Domain: immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;132-191/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: NCAM
   Query Match
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                                                                          316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and immunological characterization of the amino-terminal A44290; MUID:86140120; PMID:3512556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell-cell adhesion via homophilic binding with and of NCAM are produced by alternative splicing. See
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   10.5%;
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8; Mismatches 86;
   Score 171.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPI-anchored splice form -
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   DB 1;
Length 725;
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   A;Gene: NCAM
A;Map position:
A;Introns: 643/
                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of
A;Reference number: A44290; MUID:86140120; PMID:3512556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Barthels, D.; Vopper, G.; Wille, W. Nucleic Acids Res. 16, 4217-4225, 1989. Nucleic Acids Res. 16, 4217-4225, 1989. A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation A;Reference number: S00382; MUID:88283628; PMID:3398534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,'L'
A;Residues: 1-548,'T',550-571,'NID:953342; PIDN:CAA68263.1; PID:953343
A;Cross-references: EMBL:Y00051; NID:953342; PIDN:CAA68263.1; PID:953343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
A;Reference number: S00844; MUID:88067687; PMID:3684567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA A;Reference number: A29673; MUID:87246524; PMID:3595563 A;Accession: A29673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 31-Dec-2000
C;Accession: A29673; S00844; S0084; A28281; A44290; S00383
C;Accession: A29673; S00844; Fulle, W.; Ruppert, C.; Chaix, J.C.; Hirsch, R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, EMBO J. 6, 907-914, 1987
                                                                                                                 C; Comment:
C; Genetics:
                                                                                                                                                                                            A;Residues:
C;Comment: 1
                                                                                                                                                                                                                                                               A;Reference number: A44290;
A;Accession: A44290
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 804-1081 <BA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; R;Rougon, G.; Marshak, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 529-809, 1077-1115 <SAN>
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                                                                                                                                                     Comment: NCAM mediates
Comment: Several forms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 VIELTVQVKPVTPVCR---VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN
   643/3; 701/1; 770/2; 809/2; 1076/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
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                                                                                                                                                                                                                               20-36 <ROU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D
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                                                                                                                                                     cell-cell adhesion via homophilic binding with another NCAM mol of NCAM are produced by alternative splicing. See also PIR:IJMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SDSSEVTIRNVDKNDEAEYVCIAENKAG----EQDASIH
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1; Mismatches
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; T88136
R;Small, S.J; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence A;Reference number: S00846; MUID:88059265; PMID:3680385
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                                                 A; Title: Polypeptide variation in an N-CAM
A; Reference number: I58136; MUID: 90166485;
                                                                                                                                                                                                                                      R;Small, S.J.; Akeson, R.

J. Cell Biol. 111, 2089-2096, 1990

A;Title: Expression of the unique NCAM VASE exon is independently regulated in A;Reference number: A37795; MUID:91035620; PMID:1699951

A;Accession: B37795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural cell adhesion molecule short domain form N;Alternate names: NCAM-140
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F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;20-711/Domain: extracellular #status predicted <EXT>F;34-98/Domain: immunoglobulin homology <IMM1>F;132-191/Domain: immunoglobulin homology <IMM2>
                                                                                                     R;Small, S.J.; Haines, S.L.;
Neuron 1, 1007-1017, 1988
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X06564 R;Small, S.J.; Akeson, R.
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-858 < SMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;161-165/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;152-156/Region:
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                A; Accession: I58136
                                                                                                                                                              A;Residues:
                                                                                                                                                                                       A;Molecule type: mRNA
                                                                                                                                                                                                             A; Status: preliminary; not
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-729/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,316,348,424,450,479/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                              340-381 <SM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      S00846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLIGA------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ
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heparin binding #status predicted
immunoglobulin homology <IMM3>
NCAM binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin homology <IMM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibronectin type III repeat homology <FN3A> fibronectin type III repeat homology <FN3B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%;
                                                                                                                                                                                                             compared with conceptual translation
                                                                                                                                Akeson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 171.5; DB 1;
Pred. No. 5e-06;
                                                                                                                                   æ
                                                      extracellular
PMID:2483093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1115
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                                                                               immunoglobulin-like fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQDASIH 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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A;Gene:
C;Superf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;430-492/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;323-398/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;228-290/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;132-191/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;20-858/Product: neural
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F;1-19/Domain: signal sequence #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;722-739/Domain: transmembrane #status predicted <TMM>;722-739/Domain: intracellular #status predicted <INT>;40-858/Domain: intracellular #status predicted <INT>;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;1-19/Domain: signal sequence #status predicted <SIG>;20-858/Product: neural cell adhesion molecule, short;20-721/Domain: extracellular #status predicted <EXT>;20-721/Domain: extracellular #status predicted <EXT>;20-721/Domain: demandation for the status predicted <EXT>;24-08/Domain: demandation for the status predicted <EXT>;25-08/Domain: demandation for the status predicted <EXT>;25-08/Do
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          188
                                                                                                              203
                                                                                                                                                                                                   130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                 72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 CLIGA-----VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
          PRFRNSSSHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY
                                                                                                              DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE---
                                                                                                                                                                                                                                                                                                            ----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heparin binding #status predicted heparin binding #status predicted immunoglobulin homology <IMM3>
NCAM binding #status predicted immunoglobulin homology <IMM4>
immunoglobulin homology <IMM4>
immunoglobulin homology <IMM5>
fibronectin type III repeat homology <FN3A>
fibronectin type III repeat homology <FN3B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin homology < IMM2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%;
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Pred. No. 4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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rin binding; si
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---EDDEKHIFSDDSSELTIRNVDKNDEAEYVCIAENKAG----EQDASIH

C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #text_change 21-Jan-2000
C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56178; \$12052; \$44929
R;Pulldo, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphat protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor N,Alternate_names: protein-tyrosine-phosphatase BPTP-2

ase delta isoforms. A;Reference number: A56178; A;Accession: A56178 MUID:95204468; PMID:7896816

A;Status: preliminary

PIDN:AAC41749.1; PID:g755653

A;Molecule type: mRNA A;Residues: 1-1912 <PULS A;Residues: 1-1912 <PULS A;Crooss-references: GB:L18929; NID:g755652; R;Krueger, N.X.; Streuli, M.; Saito, H. EMBO J. 9, 3241-3252, 1990 A;Tille: Structural diversity and evolution A;Reference number: S12049; MUID:91006018; P A; Accession: S12052 of human receptor-like protein tyrosine PMID:2170109 Boud

A;Status: purcham A;Molecule type: mRNĀ A;Residues: 390-1912 <KRU> A;Cross-references: GB:X54133; A;Cross-rho sequence from Fig. NID:g35789; PIDN:CAA38068.1; PID:g35790 5B is inconsistent with that from Fig. 5A in having 568-T

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F;140-209/Domain: immunoglobulin homology <IMM2>
F;250-304/Domain: immunoglobulin homology <IMM3>
F;711-811/Domain: fibronectin type III repeat homology <3FR>
F;711-812/Domain: fibronectin type III repeat homology <3FR>
F;1293-1912/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1559/Binding site: substrate phosphate (Arg) #status predicted
F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1850/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1756-1804,'C',1806-1845 <ADA>
A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
A;Experimental source: pre-B cell NALM-6
A;Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
                                                                                           R;Chou, Y.H.; Hayman, M.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991

A;Title: Characterization of a member of the immunoglobulin gene superfam A;Reference number: A39712; MUID:91271300; PMID:1711213

A;Accession: A39712

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1051 <CHO>
A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein c;Keywords: ATP:
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein c;Keywords: ATP:
C;Superfamily: protein kinase homology <KIN>
F;783-791/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                    kinase-like protein klg precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999 C;Accession: A39712 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A39712
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C; Superfamily: leukocyte
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Cancer Res. 52,
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A;Reference number: A44929; MUID:92119637; PMID:1370651
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Query Match
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Conservative
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28.6%; Pred. No. 1.4e-05;
tive 35; Mismatches 76
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                      10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSE
Score 164.5;
Pred. No. 1.8e
35; Mismatches
  1.8e-05;
ches 109;
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-3707 < NOO>
A; Residues: 1-3707 < NOO>
A; Cross-references: EMBL: M77174; .NID: g200295; PIDN: AAA39911.1; PID: g200296
A; Cross-references: EMBL: M77174; .NID: g200295; PIDN: AAA39911.1; PID: g200296
R; Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass
J. Biol. Chem. 263, 16379-16387, 1988
J. Biol. Chem. 263, 16379-16387, 1988
J. Biol. Chem. 263, 16379-16387, 1988
A; Title: Identification of cDNA clones encoding different domains of the basement membra
A; Title: Identification of cDNA clones encoding different domains of the basement membra
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A;Molecule type: protein
A;Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
A;Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>
C;Superfamily: LDL receptor ligand-binding repeat l
C;Keywords: glycoprotein
C;Keywords: glycoprotein
C;Keywords: glycoprotein
C;Keywords: glycoprotein
C;Keywords: glycoprotein
C;Keywords: glycoprotein
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R;Schulze, B; Mann, K; Battistutta, R.; Wiedemann, H.; Timpl,
Bur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of particles for the combinant domain III-3 of particles for the
                                                                                                                                                                                                                                                                                              F;1159-1206/Domain: laminin-type EGF-like homology <LEG7> F;1563-1610/Domain: laminin-type EGF-like homology <EG7> F;1613-1668/Domain: laminin-type EGF-like homology <LEG8> F;1613-1694/Domain: BGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;199-234/Domain: LDL receptor ligand-binding repeat he F;285-319/Domain: LDL receptor ligand-binding repeat he F;285-319/Domain: LDL receptor ligand-binding repeat he F;368-403/Domain: LDL receptor ligand-binding repeat he F;368-403/Domain: LDL receptor ligand-binding repeat he F;368-403/Domain: Laminin-type EGF-like homology <LEGo-
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A; Residues: 1870-2600 < NO3>
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A; Residues: 940-1601 < NO2>
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A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate padhesion molecule.
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
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N;Alternate name
                                                                                               F;3163-3198/Domain: EGF homology <EGF>F;3270-3423/Domain: laminin G repeat homology <LG2>F;3270-3423/Domain: EGF homology <EGF7>F;3464-3492/Domain: EGF homology <EGF7>F;1256,1891,2336,2394,2427/Binding site: carbohydra
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F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:268-288/Domain: immunoglobulin homology <IMM3>
F:268-270/Region: NCAM binding #status predicted
F:361-270/Region: NCAM binding #status predicted
F:361-370/Region: immunoglobulin homology <IMM4>
F:428-490/Domain: immunoglobulin homology <IMM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Roesidues: 20-36 <ROU>
A;Roesidues: 20-36 <ROU>
A;Note: 23-Glu was also found
A;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM πC;Comment: Various forms of NCAM are produced by alternative splicing.
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; in C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Rougon,
J. Biol. (
                                                                                                       F;720-737/Domain: transmembrane #status predicted <TMM>
F;738-853/Domain: intracellular #status predicted <INT>
F;738-853/Domain: intracellular #status predicted conds: #status predicted
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                     F;1-19/Domain: signal sequence #status predicted <SIG>F;20-853/Product: neural cell adhesion molecule, short F;20-719/Domain: extracellular #status predicted <EXT>F;34-98/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Structural and immunological characterization of the amino-terminal domain of A;Reference number: A44290; MUID:86140120; PMID:3512556 A;Accession: B44290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562 A;Note: the authors identified this protein as calmodulin-independent adenylate cyclase R;Rougon, G.; Marshak, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence
A;Reference number: A32976; MUID:89378239; PMID:2776887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; A38778; B44290; S05402
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IJBONC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural cell adhesion molecule short domain form N; Alternate names: NCAM-140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A32976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, FEBS Lett. 254, 69-73, 1989
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                                                                                                                                                                                    ;633-693/Domain:
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                       10.0%;
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5; Mismatches 74;
                       Score 163.5;
Pred. No. 1.7
                                                                                           site: carbohydrate (Asn)
       Mismatches
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                  .7e-05
                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    short domain
                                            Length 853;
    Indels
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                                                                                         (covalent)
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    45;
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Gaps
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T29757
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Best Local
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A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2;
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-6642 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89 A;Experimental source: strain Bristol N2; clone C09D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z20679
A; Accession: T29757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Caenorhabditis elegans;
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999;
                                                                                                                                                                                                                                                                                                                                                                            3884 -----TLTFDNVTQADAGEYRCEAENEYGSAWTEGPIIVTLEGAPKIDGEAPDFLQPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 EFESVELSCIITDSQTS------DPRIEWKK--IQDEQTTYVFFDNKIQGDLAGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
RVHFESTDDGTQRLVIEDSKTDDQGNYR
                                                                                                                                                                                  DGTQRLTVTNAKLDDMDEYRCEASNEFGDVWSDVTLTVKEPAQVAPGFFKELSAIQVKET
                                                                                                                                                                                                                                 SETGTLVFTAVHKDDSGQYYCIASNDAG----
                                                                                                                                                                                                                                                                                                                           PVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLN
                                                                                                                                                                                                                                                                                                                                                                                                                         EILGKTSLKIWNVTRRDSALYRCE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFVELLRSCTVTEKQQAILKCKVKGEPRPKIKWTKEGKEVEMSARVRAEHKDDGTL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLFSDDSSE-----LTIRKVDKNDEAEYVCIAENKAG-----EQDASIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY
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                                                                                          ETAKFECKVSG-
                                                                                                                                    EMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKP-----
                                                                                                                                                                                                                                                                               PA------KPSDRVKIENLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVVTAEDGTESEATVNVKIFQKLMFKNAPTPQEFREGEDAVIVCDVVSSLPPTIIWK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence
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                                            DGVNYI - - - - RTDEEGDFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 162.5; DB 2
Pred. No. 0.00024;
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6609/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6642;
                                                                                          TKPDVKWFKD-GTPLKEDK 407:
                                                                                                                                                                                                                                   ---SARCEEQ 233
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